Rahul Satija

List of Publications by Year
in descending order

63	60,887	44069 48	114465 63
papers	citations	h-index	g-index

86	86	86	64143
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolutionary systems biology reveals patterns of rice adaptation to drought-prone agro-ecosystems. Plant Cell, 2022, 34, 759-783.	6.6	19
2	Comparison and evaluation of statistical error models for scRNA-seq. Genome Biology, 2022, 23, 27.	8.8	140
3	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. Nature Biotechnology, 2022, 40, 1220-1230.	17.5	46
4	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	6.5	58
5	Characterizing the molecular regulation of inhibitory immune checkpoints with multimodal single-cell screens. Nature Genetics, 2021, 53, 322-331.	21.4	96
6	A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness. Nature Immunology, 2021, 22, 723-734.	14.5	26
7	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29.	28.9	5,912
8	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	17.5	244
9	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
10	Single-cell chromatin state analysis with Signac. Nature Methods, 2021, 18, 1333-1341.	19.0	595
11	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. Genome Biology, 2021, 22, 333.	8.8	15
12	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. Nature Communications, 2020, 11, 5504.	12.8	39
13	Niche-Selective Inhibition of Pathogenic Th17 Cells by Targeting Metabolic Redundancy. Cell, 2020, 182, 641-654.e20.	28.9	77
14	The strength and pattern of natural selection on gene expression in rice. Nature, 2020, 578, 572-576.	27.8	92
15	3017 â€" A DISTINCT SUBSET OF LATENT LONG-TERM HUMAN HEMATOPOIETIC STEM CELLS RESISTS REGENERATIVE STRESS TO PRESERVES STEMNESS. Experimental Hematology, 2020, 88, S43.	0.4	0
16	Divergent Levels of CD112 and INKA1 Define a Subset of Human Hematopoietic Stem Cells That Resists Regenerative Stress to Preserve Stemness. Blood, 2020, 136, 5-5.	1.4	0
17	Integrative single-cell analysis. Nature Reviews Genetics, 2019, 20, 257-272.	16.3	932
18	Comprehensive Integration of Single-Cell Data. Cell, 2019, 177, 1888-1902.e21.	28.9	9,755

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19	A single-cell transcriptional roadmap for cardiopharyngeal fate diversification. Nature Cell Biology, 2019, 21, 674-686.	10.3	78
20	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. Nature Methods, 2019, 16, 409-412.	19.0	364
21	The bone marrow microenvironment at single-cell resolution. Nature, 2019, 569, 222-228.	27.8	624
22	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression. Genome Biology, 2019, 20, 296.	8.8	2,460
23	Toward a Common Coordinate Framework for the Human Body. Cell, 2019, 179, 1455-1467.	28.9	81
24	Single-cell RNA-seq of rheumatoid arthritis synovial tissue using low-cost microfluidic instrumentation. Nature Communications, 2018, 9, 791.	12.8	284
25	Developmental diversification of cortical inhibitory interneurons. Nature, 2018, 555, 457-462.	27.8	393
26	Strength in numbers from integrated single-cell neuroscience. Nature Biotechnology, 2018, 36, 41-42.	17.5	1
27	Integrating single-cell transcriptomic data across different conditions, technologies, and species. Nature Biotechnology, 2018, 36, 411-420.	17.5	8,878
28	Molecular transitions in early progenitors during human cord blood hematopoiesis. Molecular Systems Biology, 2018, 14, e8041.	7.2	125
29	Single-cell RNA sequencing to explore immune cell heterogeneity. Nature Reviews Immunology, 2018, 18, 35-45.	22.7	1,085
30	Cell Hashing with barcoded antibodies enables multiplexing and doublet detection for single cell genomics. Genome Biology, 2018, 19, 224.	8.8	674
31	Kinetics of adult hematopoietic stem cell differentiation in vivo. Journal of Experimental Medicine, 2018, 215, 2815-2832.	8.5	61
32	Phenotypic Convergence: Distinct Transcription Factors Regulate Common Terminal Features. Cell, 2018, 174, 622-635.e13.	28.9	180
33	Seq-Well: portable, low-cost RNA sequencing of single cells at high throughput. Nature Methods, 2017, 14, 395-398.	19.0	706
34	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	12.6	1,846
35	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
36	Simultaneous epitope and transcriptome measurement in single cells. Nature Methods, 2017, 14, 865-868.	19.0	2,124

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37	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
38	Root Regeneration Triggers an Embryo-like Sequence Guided by Hormonal Interactions. Cell, 2016, 165, 1721-1733.	28.9	215
39	Human dendritic cells (DCs) are derived from distinct circulating precursors that are precommitted to become CD1c+ or CD141+ DCs. Journal of Experimental Medicine, 2016, 213, 2861-2870.	8.5	124
40	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
41	Single-cell analysis reveals key roles for Bcl11a in regulating stem cell fate decisions. Genome Biology, 2015, 16, 199.	8.8	11
42	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. Cell, 2015, 161, 1202-1214.	28.9	5,908
43	MERFISHing for spatial context. Trends in Immunology, 2015, 36, 390-391.	6.8	6
44	A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians. Developmental Cell, 2015, 35, 632-645.	7.0	184
45	Dynamic profiling of the protein life cycle in response to pathogens. Science, 2015, 347, 1259038.	12.6	408
46	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	28.9	383
47	Spatial reconstruction of single-cell gene expression data. Nature Biotechnology, 2015, 33, 495-502.	17.5	4,254
48	Pathogen Cell-to-Cell Variability Drives Heterogeneity in Host Immune Responses. Cell, 2015, 162, 1309-1321.	28.9	255
49	The Regulatory Factor ZFHX3 Modifies Circadian Function in SCN via an AT Motif-Driven Axis. Cell, 2015, 162, 607-621.	28.9	74
50	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. Cell, 2015, 163, 1400-1412.	28.9	504
51	Deconstructing transcriptional heterogeneity in pluripotent stem cells. Nature, 2014, 516, 56-61.	27.8	343
52	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
53	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. Cell, 2014, 159, 148-162.	28.9	770
54	Heterogeneity in immune responses: from populations to single cells. Trends in Immunology, 2014, 35, 219-229.	6.8	166

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55	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. Nature, 2014, 510, 363-369.	27.8	872
56	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. Cell, 2013, 155, 1409-1421.	28.9	554
57	Dynamic regulatory network controlling TH17 cell differentiation. Nature, 2013, 496, 461-468.	27.8	608
58	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. Nature, 2013, 498, 236-240.	27.8	1,103
59	Comparative analysis of RNA sequencing methods for degraded or low-input samples. Nature Methods, 2013, 10, 623-629.	19.0	419
60	The Atypical Calpains: Evolutionary Analyses and Roles in Caenorhabditis elegans Cellular Degeneration. PLoS Genetics, 2012, 8, e1002602.	3.5	23
61	The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the <i>Drosophila</i> embryo. Genome Research, 2012, 22, 656-665.	5.5	44
62	Stochastic models of sequence evolution including insertion–deletion events. Statistical Methods in Medical Research, 2009, 18, 453-485.	1.5	22
63	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i>. Science, 2006, 314, 941-952.	12.6	1,018